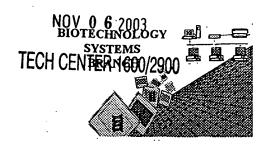# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/009,792 B_

Source: _1600_

Date Processed by STIC: _10/23/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

1600

RAW SEQUENCE LISTING   DATE: 10/23/2003
PATENT APPLICATION: US/10/009,792B   TIME: 11:13:03

Input Set : **A:\hylee60seql.txt**
Output Set: **N:\CRF4\10232003\J009792B.raw**

```
 4 <110> APPLICANT: LEE, Sang-Yup
 5         JEONG, Ki-Jun
 7 <120> TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
 8         GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
11 <130> FILE REFERENCE: HYLEE60.001APC
13 <140> CURRENT APPLICATION NUMBER: US 10/009,792B
14 <141> CURRENT FILING DATE: 2001-12-13
16 <150> PRIOR APPLICATION NUMBER: PCT/KR01/00549
17 <151> PRIOR FILING DATE: 2001-03-31
19 <150> PRIOR APPLICATION NUMBER: KR 10-2000-0017052
20 <151> PRIOR FILING DATE: 2000-03-31
22 <160> NUMBER OF SEQ ID NOS: 30
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
402 <210> SEQ ID NO: 30
403 <211> LENGTH: 14
404 <212> TYPE: PRT
405 <213> ORGANISM: synthetic sequence
407 <400> SEQUENCE: 30
408 Ala Gly Pro His His His His His Ile Glu Gly Arg Thr
409 1               5                       10
E--> 413 S:\DOCS\SGJ\HYLEE60-SL.TXT
E--> 414 100903
E--> 415 1
E--> 416 9
```

[handwritten annotations:] invalid; response – see item 10 on Error Summary Sheet (this error also appears in sequences 28-29)

[handwritten:] pp 1-2

Does Not Comply
Corrected Diskette Needed

[handwritten:] delete

[handwritten:] see p-2, too

<210> 1
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Oligopeptide   give source of genetic material – see Item 11

on Error
Summary Sheet

<400> 1
Ala Gly Pro His His His His His His Ile Glu Gly Arg
 1   5   10

Input Set : **A:\hylee60seq1.txt**
Output Set: **N:\CRF4\10232003\J009792B.raw**

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:413 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:413 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:414 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
M:332 Repeated in SeqNo=30
L:418 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:15 SEQ:30